



# SEQUENCE LISTING

<110> Raines, Ronald T

<120> Oxidation-Resistant Ribonuclease Inhibitor

<130> 960296.95360

<140> 09/234,028

<141> 1999-01-20

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 456

<212> PRT

<213> Rattus sp.

<400> 1

Met Ser Leu Asp Ile Gln Cys Glu Gln Leu Ser Asp Ala Arg Trp Thr  
1 5 10 15

Glu Leu Leu Pro Leu Ile Gln Gln Tyr Gln Val Val Arg Leu Asp Asp  
20 25 30

Cys Gly Leu Thr Glu Val Arg Cys Lys Asp Ile Arg Ser Ala Ile Gln  
35 40 45

Ala Asn Pro Ala Leu Thr Glu Leu Ser Leu Arg Thr Asn Glu Leu Gly  
50 55 60

Asp Ala Gly Val Gly Leu Val Leu Gln Gly Leu Gln Asn Pro Thr Cys  
65 70 75 80

Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Ser Leu Thr Glu Ala Gly  
85 90 95

Cys Gly Val Leu Pro Asp Val Leu Arg Ser Leu Ser Thr Leu Arg Glu  
100 105 110

Leu His Leu Asn Asp Asn Pro Leu Gly Asp Glu Gly Leu Lys Leu Leu  
115 120 125

Cys Glu Gly Leu Arg Asp Pro Gln Cys Arg Leu Glu Lys Leu Gln Leu  
130 135 140

Glu Tyr Cys Asn Leu Thr Ala Thr Ser Cys Glu Pro Leu Ala Ser Val			
145	150	155	160
Leu Arg Val Lys Pro Asp Phe Lys Glu Leu Val Leu Ser Asn Asn Asp			
	165	170	175
Phe His Glu Ala Gly Ile His Thr Leu Cys Gln Gly Leu Lys Asp Ser			
	180	185	190
Ala Cys Gln Leu Glu Ser Leu Lys Leu Glu Asn Cys Gly Ile Thr Ser			
	195	200	205
Ala Asn Cys Lys Asp Leu Cys Asp Val Val Ala Ser Lys Ala Ser Leu			
	210	215	220
Gln Glu Leu Asp Leu Gly Ser Asn Lys Leu Gly Asn Thr Gly Ile Ala			
225	230	235	240
Ala Leu Cys Ser Gly Leu Leu Leu Pro Ser Cys Arg Leu Arg Thr Leu			
	245	250	255
Trp Leu Trp Asp Cys Asp Val Thr Ala Glu Gly Cys Lys Asp Leu Cys			
	260	265	270
Arg Val Leu Arg Ala Lys Gln Ser Leu Lys Glu Leu Ser Leu Ala Gly			
	275	280	285
Asn Glu Leu Lys Asp Glu Gly Ala Gln Leu Leu Cys Glu Ser Leu Leu			
	290	295	300
Glu Pro Gly Cys Gln Leu Glu Ser Leu Trp Val Lys Thr Cys Ser Leu			
305	310	315	320
Thr Ala Ala Ser Cys Pro His Phe Cys Ser Val Leu Thr Lys Asn Ser			
	325	330	335
Ser Leu Phe Glu Leu Gln Met Ser Ser Asn Pro Leu Gly Asp Ser Gly			
	340	345	350
Val Val Glu Leu Cys Lys Ala Leu Gly Tyr Pro Asp Thr Val Leu Arg			
	355	360	365
Val Leu Trp Leu Gly Asp Cys Asp Val Thr Asp Ser Gly Cys Ser Ser			
	370	375	380
Leu Ala Thr Val Leu Leu Ala Asn Arg Ser Leu Arg Glu Leu Asp Leu			
385	390	395	400

Ser Asn Asn Cys Met Gly Asp Asn Gly Val Leu Gln Leu Leu Glu Ser  
405 410 415

Leu Lys Gln Pro Ser Cys Ile Leu Gln Gln Leu Val Leu Tyr Asp Ile  
420 425 430

Tyr Trp Thr Asp Glu Val Glu Asp Gln Leu Arg Ala Leu Glu Glu Glu  
435 440 445

Arg Pro Ser Leu Arg Ile Ile Ser  
450 455

<210> 2  
<211> 456  
<212> PRT  
<213> Sus sp.

<400> 2  
Met Asn Leu Asp Ile His Cys Glu Gln Leu Ser Asp Ala Arg Trp Thr  
1 5 10 15

Glu Leu Leu Pro Leu Leu Gln Gln Tyr Glu Val Val Arg Leu Asp Asp  
20 25 30

Cys Gly Leu Thr Glu Glu His Cys Lys Asp Ile Gly Ser Ala Leu Arg  
35 40 45

Ala Asn Pro Ser Leu Thr Glu Leu Cys Leu Arg Thr Asn Glu Leu Gly  
50 55 60

Asp Ala Gly Val His Leu Val Leu Gln Gly Leu Gln Ser Pro Thr Cys  
65 70 75 80

Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Ser Leu Thr Glu Ala Gly  
85 90 95

Cys Gly Val Leu Pro Ser Thr Leu Arg Ser Leu Pro Thr Leu Arg Glu  
100 105 110

Leu His Leu Ser Asp Asn Pro Leu Gly Asp Ala Gly Leu Arg Leu Leu  
115 120 125

Cys Glu Gly Leu Leu Asp Pro Gln Cys His Leu Glu Lys Leu Gln Leu  
130 135 140

Glu Tyr Cys Arg Leu Thr Ala Ala Ser Cys Glu Pro Leu Ala Ser Val  
145 150 155 160

Leu Arg Ala Thr Arg Ala Leu Lys Glu Leu Thr Val Ser Asn Asn Asp	165	170	175
Ile Gly Glu Ala Gly Ala Arg Val Leu Gly Gln Gly Leu Ala Asp Ser	180	185	190
Ala Cys Gln Leu Glu Thr Leu Arg Leu Glu Asn Cys Gly Leu Thr Pro	195	200	205
Ala Asn Cys Lys Asp Leu Cys Gly Ile Val Ala Ser Gln Ala Ser Leu	210	215	220
Arg Glu Leu Asp Leu Gly Ser Asn Gly Leu Gly Asp Ala Gly Ile Ala	225	230	235
Glu Leu Cys Pro Gly Leu Leu Ser Pro Ala Ser Arg Leu Lys Thr Leu	245	250	255
Trp Leu Trp Glu Cys Asp Ile Thr Ala Ser Gly Cys Arg Asp Leu Cys	260	265	270
Arg Val Leu Gln Ala Lys Glu Thr Leu Lys Glu Leu Ser Leu Ala Gly	275	280	285
Asn Lys Leu Gly Asp Glu Gly Ala Arg Leu Leu Cys Glu Ser Leu Leu	290	295	300
Gln Pro Gly Cys Gln Leu Glu Ser Leu Trp Val Lys Ser Cys Ser Leu	305	310	315
Thr Ala Ala Cys Cys Gln His Val Ser Leu Met Leu Thr Gln Asn Lys	325	330	335
His Leu Leu Glu Leu Gln Leu Ser Ser Asn Lys Leu Gly Asp Ser Gly	340	345	350
Ile Gln Glu Leu Cys Gln Ala Leu Ser Gln Pro Gly Thr Thr Leu Arg	355	360	365
Val Leu Cys Leu Gly Asp Cys Glu Val Thr Asn Ser Gly Cys Ser Ser	370	375	380
Leu Ala Ser Leu Leu Leu Ala Asn Arg Ser Leu Arg Glu Leu Asp Leu	385	390	395
Ser Asn Asn Cys Val Gly Asp Pro Gly Val Leu Gln Leu Leu Gly Ser	405	410	415

Leu Glu Gln Pro Gly Cys Ala Leu Glu Gln Leu Val Leu Tyr Asp Thr  
 420 425 430

Tyr Trp Thr Glu Glu Val Glu Asp Arg Leu Gln Ala Leu Glu Gly Ser  
 435 440 445

Lys Pro Gly Leu Arg Val Ile Ser  
 450 455

<210> 3  
 <211> 461  
 <212> PRT  
 <213> Homo sapiens

<400> 3  
 Met Ser Leu Asp Ile Gln Ser Leu Asp Ile Gln Cys Glu Glu Leu Ser  
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Asp Ala Arg Trp Ala Glu Leu Leu Pro Leu Leu Gln Gln Cys Gln Val  
 20 25 30

Val Arg Leu Asp Asp Cys Gly Leu Thr Glu Ala Arg Cys Lys Asp Ile  
 35 40 45

Ser Ser Ala Leu Arg Val Asn Pro Ala Leu Ala Glu Leu Asn Leu Arg  
 50 55 60

Ser Asn Glu Leu Gly Asp Val Gly Val His Cys Val Leu Gln Gly Leu  
 65 70 75 80

Gln Thr Pro Ser Cys Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Cys  
 85 90 95

Leu Thr Gly Ala Gly Cys Gly Val Leu Ser Ser Thr Leu Arg Thr Leu  
 100 105 110

Pro Thr Leu Gln Glu Leu His Leu Ser Asp Asn Leu Leu Gly Asp Ala  
 115 120 125

Gly Leu Gln Leu Leu Cys Glu Gly Leu Leu Asp Pro Gln Cys Arg Leu  
 130 135 140

Glu Lys Leu Gln Leu Glu Tyr Cys Ser Leu Ser Ala Ala Ser Cys Glu  
 145 150 155 160

Pro Leu Ala Ser Val Leu Arg Ala Lys Pro Asp Phe Lys Glu Leu Thr

	165		170		175
Val Ser Asn Asn Asp Ile Asn Glu Ala Gly Val Arg Val Leu Cys Gln					
	180		185		190
Gly Leu Lys Asp Ser Pro Cys Gln Leu Glu Ala Leu Lys Leu Glu Ser					
	195		200		205
Cys Gly Val Thr Ser Asp Asn Cys Arg Asp Leu Cys Gly Ile Val Ala					
	210		215		220
Ser Lys Ala Ser Leu Arg Glu Leu Ala Leu Gly Ser Asn Lys Leu Gly					
	225		230		235
Asp Val Gly Met Ala Glu Leu Cys Pro Gly Leu Leu His Pro Ser Ser					
	245		250		255
Arg Leu Arg Thr Leu Trp Ile Trp Glu Cys Gly Ile Thr Ala Lys Gly					
	260		265		270
Cys Gly Asp Leu Cys Arg Val Leu Arg Ala Lys Glu Ser Leu Lys Glu					
	275		280		285
Leu Ser Leu Ala Gly Asn Glu Leu Gly Asp Glu Gly Ala Arg Leu Leu					
	290		295		300
Cys Glu Thr Leu Leu Glu Pro Gly Cys Gln Leu Glu Ser Leu Trp Val					
	305		310		315
Lys Ser Cys Ser Phe Thr Ala Ala Cys Cys Ser His Phe Ser Ser Val					
	325		330		335
Leu Ala Gln Asn Arg Phe Leu Leu Glu Leu Gln Ile Ser Asn Asn Arg					
	340		345		350
Leu Glu Asp Ala Gly Val Arg Glu Leu Cys Gln Gly Leu Gly Gln Pro					
	355		360		365
Gly Ser Val Leu Arg Val Leu Trp Leu Ala Asp Cys Asp Val Ser Asp					
	370		375		380
Ser Ser Cys Ser Ser Leu Ala Ala Thr Leu Leu Ala Asn His Ser Leu					
	385		390		395
Arg Glu Leu Asp Leu Ser Asn Asn Cys Leu Gly Asp Ala Gly Ile Leu					
	405		410		415
Gln Leu Val Glu Ser Val Arg Gln Pro Gly Cys Leu Leu Glu Gln Leu					

420	425	430
Val Leu Tyr Asp Ile Tyr Trp Ser Glu Glu Met Glu Asp Arg Leu Gln		
435	440	445
Ala Leu Glu Lys Asp Lys Pro Ser Leu Arg Val Ile Ser		
450	455	460

<210> 4  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: mutation  
 sequence

<400> 4  
 ggcccccgtc agcgccgcgt tctggaggct aagcttctg 39

<210> 5  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: mutation  
 sequence

<400> 5  
 gctgaagtgg ctagcggcgg cggctgtgaa 30

<210> 6  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: mutation  
 sequence

<400> 6  
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<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: mutation  
sequence

<400> 7

gctgaagtgg ctagcgcagg cggctgtgaa

30